

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: June 20, 2006, 11:43:57 ; Search time 254.305 Seconds
(without alignments)
557.351 Million cell updates/sec

Title: US-10-735-256-2_COPY_1_310
Perfect score: 310
Sequence: 1 MLPGLRLLLQAPASACLLM..... PPERQGRDLRALREADFQAC 310

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 2589679 seqs, 457216429 residues

Word size : 1

Total number of hits satisfying chosen parameters: 2588894

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : A_Geneseq_8:*
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6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*
10: geneseqp2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query					Description
	No.	Score	Match	Length	DB ID	
1	310	100.0	401	7	ADF28528	Adf28528 NgRH _y mut
2	310	100.0	420	5	AAO21477	Aao21477 Human NgR
3	310	100.0	420	6	ABR55621	Abr55621 Amino aci
4	310	100.0	420	7	ADF28510	Adf28510 NgRH _y pre
5	310	100.0	420	8	ADS10516	Ads10516 Human the
6	300	96.8	419	8	ADM72131	Adm72131 Human NTR
7	291	93.9	401	6	AAE33486	Aae33486 Human REM

8	291	93.9	401	7	ADE07875	Ade07875 Novel pro
9	280	90.3	390	5	AAO21482	Aao21482 Mature hu
10	280	90.3	390	7	ADF28529	Adf28529 NgRHy mat
11	150	48.4	512	7	ADC13559	Adc13559 Human NOV
12	141	45.5	286	8	ADT77787	Adt77787 Rat Nogo
13	141	45.5	420	6	ABR55628	Abr55628 Amino aci
14	141	45.5	420	8	ADT77788	Adt77788 Rat Nogo
15	141	45.5	452	8	ADT77808	Adt77808 Chimeric
16	141	45.5	452	8	ADT77802	Adt77802 Chimeric
17	141	45.5	474	8	ADT77796	Adt77796 Chimeric
18	133	42.9	241	4	ABG15171	Abg15171 Novel hum
19	126	40.6	807	4	ABG15173	Abg15173 Novel hum
20	56	18.1	56	4	AAM23826	Aam23826 Human EST
21	56	18.1	56	7	ADE08958	Ade08958 Novel pro
22	56	18.1	56	8	ADS11791	Ads11791 Human the
23	50	16.1	51	7	ADF28526	Adf28526 Leucine-r
24	44	14.2	114	2	AAY10843	Aay10843 Amino aci
25	44	14.2	114	7	ADB47833	Adb47833 Novel hum
26	44	14.2	114	8	ADJ55388	Adj55388 Novel hum
27	44	14.2	114	9	AED67371	Aed67371 Human imm
28	33	10.6	492	4	ABG15172	Abg15172 Novel hum
29	30	9.7	30	7	ADF28512	Adf28512 NgRHy sig
30	25	8.1	25	7	ADF28520	Adf28520 Leucine-r
31	24	7.7	24	7	ADF28524	Adf28524 Leucine-r
32	24	7.7	24	7	ADF28525	Adf28525 Leucine-r
33	24	7.7	24	7	ADF28523	Adf28523 Leucine-r
34	24	7.7	24	7	ADF28522	Adf28522 Leucine-r
35	24	7.7	24	7	ADF28519	Adf28519 Leucine-r
36	24	7.7	24	7	ADF28521	Adf28521 Leucine-r
37	22	7.1	22	7	ADF28518	Adf28518 Leucine-r
38	15	4.8	15	7	ADF28513	Adf28513 PR00019A
39	15	4.8	15	7	ADF28515	Adf28515 PR00019A
40	15	4.8	15	7	ADF28516	Adf28516 PR00019B
41	15	4.8	15	7	ADF28514	Adf28514 PR00019B
42	15	4.8	15	7	ADF28517	Adf28517 PR00019B
43	11	3.5	11	8	ADT77816	Adt77816 Rat Nogo
44	11	3.5	49	6	ABR62021	Abr62021 Mouse Nog
45	11	3.5	49	6	ABR62022	Abr62022 Rat Nogo

ALIGNMENTS

RESULT 1
 ADF28528
 ID ADF28528 standard; protein; 401 AA.
 XX
 AC ADF28528;
 XX
 DT 12-FEB-2004 (first entry)
 XX
 DE NgRHy mutant protein lacking transmembrane domain - SED ID 438.
 XX
 KW neuroprotective; nootropic; cerebroprotective; antiparkinsonian;
 KW neurological; spinal cord injury; cranial; cerebral trauma; stroke;
 KW Alzheimer's disease; anxiety; autism; Parkinson's; tardive dyskinesia;
 KW paralysis; seizure; memory disorder; adiponectin; Clq domain;

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OM protein - protein search, using sw model

Run on: June 20, 2006, 11:59:16 ; Search time 37.3051 Seconds
(without alignments)
727.367 Million cell updates/sec

Title: US-10-735-256-2_COPY_1_310
Perfect score: 310
Sequence: 1 MLPGLRRLLQAPASACLLM.....PPERQGRDLRALREADFQAC 310

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 650591 seqs, 87530628 residues

Word size : 1

Total number of hits satisfying chosen parameters: 649019

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued_Patents_AA:
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3: /EMC_Celerra_SIDS3/ptodata/2/iaa/7_COMB.pep:
4: /EMC_Celerra_SIDS3/ptodata/2/iaa/H_COMB.pep:
5: /EMC_Celerra_SIDS3/ptodata/2/iaa/PCTUS_COMB.pep:
6: /EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:
7: /EMC_Celerra_SIDS3/ptodata/2/iaa/backfiles1.pep:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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		Match	Length	DB	
1	44	14.2	115	2	US-09-774-639-154 Sequence 154, App
2	11	3.5	380	2	US-09-461-325-161 Sequence 161, App
3	11	3.5	380	2	US-10-012-542-161 Sequence 161, App
4	11	3.5	380	2	US-10-115-123-161 Sequence 161, App
5	11	3.5	473	2	US-09-949-016-8448 Sequence 8448, Ap
6	11	3.5	473	2	US-09-999-833A-400 Sequence 400, App
7	11	3.5	473	2	US-10-020-445A-400 Sequence 400, App
8	11	3.5	473	2	US-09-978-189-400 Sequence 400, App
9	11	3.5	473	2	US-10-017-085A-400 Sequence 400, App
10	11	3.5	473	3	US-10-145-129A-400 Sequence 400, App

11	11	3.5	473	3	US-10-013-929A-400	Sequence 400, App
12	11	3.5	473	3	US-10-013-917A-400	Sequence 400, App
13	8	2.6	125	2	US-09-269-410-11	Sequence 11, Appl
14	8	2.6	226	2	US-09-489-039A-10549	Sequence 10549, A
15	8	2.6	256	2	US-09-252-991A-17168	Sequence 17168, A
16	8	2.6	305	2	US-09-489-039A-7371	Sequence 7371, Ap
17	8	2.6	320	2	US-09-248-796A-16573	Sequence 16573, A
18	8	2.6	446	2	US-09-252-991A-23809	Sequence 23809, A
19	8	2.6	455	2	US-09-793-998-8	Sequence 8, Appli
20	8	2.6	799	3	US-09-396-985B-4	Sequence 4, Appli
21	8	2.6	839	3	US-09-396-985B-2	Sequence 2, Appli
22	8	2.6	839	3	US-09-396-985B-98	Sequence 98, Appl
23	8	2.6	844	2	US-09-949-016-9438	Sequence 9438, Ap
24	8	2.6	990	2	US-10-101-464A-814	Sequence 814, App
25	8	2.6	1016	2	US-09-252-991A-25429	Sequence 25429, A
26	7	2.3	30	2	US-09-402-532-9	Sequence 9, Appli
27	7	2.3	33	2	US-09-402-532-10	Sequence 10, Appl
28	7	2.3	70	2	US-09-107-532A-4266	Sequence 4266, Ap
29	7	2.3	79	2	US-09-902-540-14223	Sequence 14223, A
30	7	2.3	88	2	US-09-489-847-173	Sequence 173, App
31	7	2.3	99	2	US-09-328-352-7239	Sequence 7239, Ap
32	7	2.3	150	2	US-09-270-767-34661	Sequence 34661, A
33	7	2.3	150	2	US-09-270-767-49878	Sequence 49878, A
34	7	2.3	185	2	US-10-101-464A-519	Sequence 519, App
35	7	2.3	195	2	US-09-583-110-4761	Sequence 4761, Ap
36	7	2.3	197	2	US-09-270-767-36125	Sequence 36125, A
37	7	2.3	197	2	US-09-270-767-51342	Sequence 51342, A
38	7	2.3	198	2	US-09-107-433-4622	Sequence 4622, Ap
39	7	2.3	209	2	US-09-973-278-267	Sequence 267, App
40	7	2.3	210	2	US-09-227-357-195	Sequence 195, App
41	7	2.3	213	2	US-09-328-352-6050	Sequence 6050, Ap
42	7	2.3	222	2	US-09-248-796A-15754	Sequence 15754, A
43	7	2.3	260	2	US-09-902-540-10767	Sequence 10767, A
44	7	2.3	268	2	US-10-104-047-3172	Sequence 3172, Ap
45	7	2.3	269	2	US-09-252-991A-20218	Sequence 20218, A

ALIGNMENTS

RESULT 1

US-09-774-639-154
; Sequence 154, Application US/09774639
; Patent No. 6806351
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 90 Human Secreted Proteins
; FILE REFERENCE: PZ013P1
; CURRENT APPLICATION NUMBER: US/09/774,639
; CURRENT FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/244,112
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-02-04
; NUMBER OF SEQ ID NOS: 371
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 154
; LENGTH: 115
; TYPE: PRT

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OM protein - protein search, using sw model

Run on: June 20, 2006, 12:15:51 ; Search time 129.254 Seconds
(without alignments)
1110.962 Million cell updates/sec

Title: US-10-735-256-2_COPY_1_310
Perfect score: 310
Sequence: 1 MLPGLRRLLQAPASACLLM.....PPERQGRDLRALREADFQAC 310

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 2097797 seqs, 463214858 residues

Word size : 1

Total number of hits satisfying chosen parameters: 2096261

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Published_Applications_AA_Main:
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3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep:
4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep:
5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	310	100.0	401	5	US-10-496-905-438	Sequence 438, App
2	310	100.0	420	3	US-09-972-546-2	Sequence 2, Appli
3	310	100.0	420	5	US-10-735-256-2	Sequence 2, Appli
4	310	100.0	420	5	US-10-496-905-420	Sequence 420, App
5	310	100.0	420	5	US-10-491-810A-2	Sequence 2, Appli
6	291	93.9	401	5	US-10-477-714-17	Sequence 17, Appl
7	280	90.3	390	3	US-09-972-546-8	Sequence 8, Appli
8	280	90.3	390	5	US-10-735-256-8	Sequence 8, Appli
9	280	90.3	390	5	US-10-496-905-439	Sequence 439, App
10	150	48.4	512	4	US-10-188-248-38	Sequence 38, Appl
11	141	45.5	420	5	US-10-491-810A-25	Sequence 25, Appl

12	133	42.9	241	5	US-10-450-763-45530	Sequence 45530, A
13	126	40.6	807	5	US-10-450-763-45532	Sequence 45532, A
14	50	16.1	51	5	US-10-496-905-436	Sequence 436, App
15	44	14.2	114	3	US-09-969-730-116	Sequence 116, App
16	44	14.2	114	4	US-10-621-363-116	Sequence 116, App
17	44	14.2	114	5	US-10-986-501-116	Sequence 116, App
18	44	14.2	115	3	US-09-774-639-154	Sequence 154, App
19	33	10.6	492	5	US-10-450-763-45531	Sequence 45531, A
20	30	9.7	30	5	US-10-496-905-422	Sequence 422, App
21	25	8.1	25	5	US-10-496-905-430	Sequence 430, App
22	24	7.7	24	5	US-10-496-905-429	Sequence 429, App
23	24	7.7	24	5	US-10-496-905-431	Sequence 431, App
24	24	7.7	24	5	US-10-496-905-432	Sequence 432, App
25	24	7.7	24	5	US-10-496-905-433	Sequence 433, App
26	24	7.7	24	5	US-10-496-905-434	Sequence 434, App
27	24	7.7	24	5	US-10-496-905-435	Sequence 435, App
28	22	7.1	22	5	US-10-496-905-428	Sequence 428, App
29	15	4.8	15	5	US-10-496-905-423	Sequence 423, App
30	15	4.8	15	5	US-10-496-905-424	Sequence 424, App
31	15	4.8	15	5	US-10-496-905-425	Sequence 425, App
32	15	4.8	15	5	US-10-496-905-426	Sequence 426, App
33	15	4.8	15	5	US-10-496-905-427	Sequence 427, App
34	11	3.5	49	4	US-10-006-002-1	Sequence 1, Appli
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36	11	3.5	49	4	US-10-006-002-3	Sequence 3, Appli
37	11	3.5	49	4	US-10-127-058-1	Sequence 1, Appli
38	11	3.5	49	4	US-10-127-058-2	Sequence 2, Appli
39	11	3.5	49	4	US-10-127-058-3	Sequence 3, Appli
40	11	3.5	283	3	US-09-972-599A-55	Sequence 55, Appli
41	11	3.5	310	6	US-11-055-163-7	Sequence 7, Appli
42	11	3.5	310	6	US-11-055-163-9	Sequence 9, Appli
43	11	3.5	344	6	US-11-055-163-6	Sequence 6, Appli
44	11	3.5	344	6	US-11-055-163-8	Sequence 8, Appli
45	11	3.5	380	4	US-10-012-542-161	Sequence 161, App

ALIGNMENTS

RESULT 1

US-10-496-905-438
; Sequence 438, Application US/10496905
; Publication No. US20050192215A1
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Malabika
; APPLICANT: Tang, Y. Tom
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Wang, Zhiwei
; APPLICANT: Zhao, Qing
; APPLICANT: Xu, Chongjun
; APPLICANT: Mulero, Julio J
; APPLICANT: Boyle, Bryan J.

; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES

; FILE REFERENCE: HYS-B1CIP/US
; CURRENT APPLICATION NUMBER: US/10/496,905
; CURRENT FILING DATE: 2004-05-26

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OM protein - protein search, using sw model

Run on: June 20, 2006, 12:16:16 ; Search time 13.661 Seconds
(without alignments)
511.862 Million cell updates/sec

Title: . US-10-735-256-2_COPY_1_310
Perfect score: 310
Sequence: 1 MLPGLRLLLQAPASACLLM..... PPERQGRDLRALREADFQAC 310

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 96747 seqs, 22556637 residues

Word size : 1

Total number of hits satisfying chosen parameters: 96734

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

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5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*

6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10_NEW_PUB.pep:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query			Description
		Match	Length	DB	
1	9	2.9	426	6	US-10-449-902-37107 Sequence 37107, A
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3	7	2.3	47	6	US-10-449-902-33749 Sequence 33749, A
4	7	2.3	50	6	US-10-449-902-33780 Sequence 33780, A
5	7	2.3	86	6	US-10-953-349-30624 Sequence 30624, A
6	7	2.3	100	6	US-10-953-349-39452 Sequence 39452, A
7	7	2.3	203	6	US-10-953-349-36158 Sequence 36158, A
8	7	2.3	237	7	US-11-293-697-4647 Sequence 4647, Ap
9	7	2.3	238	6	US-10-953-349-38587 Sequence 38587, A

10	7	2.3	247	6	US-10-953-349-36157	Sequence 36157, A
11	7	2.3	278	6	US-10-953-349-4307	Sequence 4307, Ap
12	7	2.3	306	6	US-10-953-349-4306	Sequence 4306, Ap
13	7	2.3	319	6	US-10-449-902-45409	Sequence 45409, A
14	7	2.3	330	6	US-10-953-349-5740	Sequence 5740, Ap
15	7	2.3	332	6	US-10-953-349-5739	Sequence 5739, Ap
16	7	2.3	358	6	US-10-449-902-34744	Sequence 34744, A
17	7	2.3	359	6	US-10-953-349-31281	Sequence 31281, A
18	7	2.3	389	6	US-10-449-902-44348	Sequence 44348, A
19	7	2.3	434	6	US-10-471-571A-5060	Sequence 5060, Ap
20	7	2.3	470	6	US-10-953-349-31280	Sequence 31280, A
21	7	2.3	492	6	US-10-953-349-31279	Sequence 31279, A
22	7	2.3	503	6	US-10-953-349-26067	Sequence 26067, A
23	7	2.3	587	7	US-11-293-697-4811	Sequence 4811, Ap
24	7	2.3	596	6	US-10-449-902-45371	Sequence 45371, A
25	7	2.3	621	7	US-11-106-014-56	Sequence 56, Appl
26	7	2.3	692	6	US-10-196-749-560	Sequence 560, App
27	7	2.3	719	7	US-11-293-697-3841	Sequence 3841, Ap
28	7	2.3	1043	7	US-11-293-697-3097	Sequence 3097, Ap
29	7	2.3	1084	6	US-10-449-902-52915	Sequence 52915, A
30	7	2.3	1144	6	US-10-449-902-42914	Sequence 42914, A
31	6	1.9	11	7	US-11-122-986-354	Sequence 354, App
32	6	1.9	30	7	US-11-122-986-829	Sequence 829, App
33	6	1.9	36	6	US-10-449-902-39872	Sequence 39872, A
34	6	1.9	43	6	US-10-449-902-34194	Sequence 34194, A
35	6	1.9	44	7	US-11-299-304-100	Sequence 100, App
36	6	1.9	48	7	US-11-264-029-28	Sequence 28, Appl
37	6	1.9	64	6	US-10-449-902-55173	Sequence 55173, A
38	6	1.9	80	6	US-10-449-902-36288	Sequence 36288, A
39	6	1.9	83	6	US-10-449-902-35748	Sequence 35748, A
40	6	1.9	85	6	US-10-449-902-48165	Sequence 48165, A
41	6	1.9	86	6	US-10-501-834-23	Sequence 23, Appl
42	6	1.9	87	6	US-10-953-349-30981	Sequence 30981, A
43	6	1.9	92	6	US-10-953-349-25928	Sequence 25928, A
44	6	1.9	92	6	US-10-953-349-38189	Sequence 38189, A
45	6	1.9	92	6	US-10-953-349-38682	Sequence 38682, A

ALIGNMENTS

RESULT 1

US-10-449-902-37107

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; Sequence 37107, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
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OM protein - protein search, using sw model

Run on: June 20, 2006, 11:52:46 ; Search time 26.7966 Seconds
(without alignments)
1113.096 Million cell updates/sec

Title: US-10-735-256-2_COPY_1_310
Perfect score: 310
Sequence: 1 MLPGLRLLQAPASACLLM..... PPERQGRDLRALREADFQAC 310

Scoring table: OLIGO
Gapext 60.0 , Gapext 60.0

Searched: 283416 seqs, 96216763 residues

Word size : 1

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : PIR_80:*

1: pirl:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

%

Result No.	Score	Query Match	Length	DB	ID	Description
1	8	2.6	181	2	AC0550	shikimate kinase I
2	8	2.6	244	2	JC8019	CD58 protein - pig
3	8	2.6	262	1	B64154	probable radical-f
4	8	2.6	337	2	D70120	probable Na+/Ca2+-
5	8	2.6	481	2	T33733	hypothetical prote
6	8	2.6	925	2	H96638	protein T1F9.20 [i]
7	8	2.6	967	2	G96637	hypothetical prote
8	8	2.6	1148	2	D85360	hypothetical prote
9	8	2.6	1986	2	S28353	probable polyketid
10	7	2.3	60	2	AD2255	hypothetical prote
11	7	2.3	62	2	T28346	ORF MSV185 hypothe
12	7	2.3	70	2	S53706	cytochrome-c oxida
13	7	2.3	78	2	AD2707	hypothetical prote

14	7	2.3	83	2	D70639	hypothetical prote
15	7	2.3	132	1	B64104	virulence-associat
16	7	2.3	147	1	HBLUA	hemoglobin beta ch
17	7	2.3	154	2	T07767	disease resistance
18	7	2.3	154	2	T07769	disease resistance
19	7	2.3	157	2	G84292	hypothetical prote
20	7	2.3	159	2	A72679	hypothetical prote
21	7	2.3	164	2	T51261	hypothetical prote
22	7	2.3	168	2	B69776	hypothetical prote
23	7	2.3	191	2	AD0812	probable lipoprote
24	7	2.3	212	2	B75156	resolvase related
25	7	2.3	216	2	T37221	hypothetical prote
26	7	2.3	219	2	F83160	two-component resp
27	7	2.3	223	2	E83596	DNA mismatch repai
28	7	2.3	225	2	T11279	H+-transporting tw
29	7	2.3	237	2	T26765	hypothetical prote
30	7	2.3	238	2	AH0338	histidine transpor
31	7	2.3	240	1	ZIZM2	19K zein precursor
32	7	2.3	240	1	ZIZM91	19K zein precursor
33	7	2.3	240	1	ZIZM92	19K zein precursor
34	7	2.3	240	2	A22831	19K zein precursor
35	7	2.3	241	2	AG0857	hypothetical prote
36	7	2.3	250	2	S75302	hypothetical prote
37	7	2.3	252	2	T01787	thyrotropin recept
38	7	2.3	253	1	JC1319	thyrotropin recept
39	7	2.3	253	2	T00290	psiA protein - Esc
40	7	2.3	260	2	T18554	integral membrane
41	7	2.3	264	2	G83245	probable ATP-bindi
42	7	2.3	277	2	D82392	conserved hypothet
43	7	2.3	283	2	E83053	dihydropteroate sy
44	7	2.3	285	2	A40657	hypothetical prote
45	7	2.3	290	2	G95397	probable LysR-fami

ALIGNMENTS

RESULT 1

AC0550

shikimate kinase II [imported] - *Salmonella enterica* subsp. *enterica* serovar Typhi (strain CT18)

C;Species: *Salmonella enterica* subsp. *enterica* serovar Typhi

A;Note: this species has also been called *Salmonella typhi*

C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002

C;Accession: AC0550

R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, C.; Mungall, K.L.; Bentley, S.D.; Holden, M.T.G.; Sebaihia, M.; Baker, S.; Basham, D.; Brooks, K.; Chillingworth, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, J.; Feltwell, T.; Hamlin, N.; Haque, A.; Hien, T.T.; Holroyd, S.; Jagels, K.; Krogh, A.; Larsen, T.S.; Leather, S.; Moule, S.; O'Gaora, P.

Nature 413, 848-852, 2001

A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, B.G.

A;Title: Complete genome sequence of a multiple drug resistant *Salmonella enterica* serovar Typhi CT18.

A;Reference number: AB0502; MUID:21534947; PMID:11677608

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: June 20, 2006, 11:44:20 ; Search time 201.763 Seconds
(without alignments)
1421.248 Million cell updates/sec

Title: US-10-735-256-2_COPY_1_310

Perfect score: 310

Sequence: 1 MLPGLRRLLQAPASACLLLM.....PPERQGRDLRALREADFQAC 310

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 2849598 seqs, 925015592 residues

Word size : 1

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : UniProt_7.2:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	310	100.0	420	1	R4RL2_HUMAN	Q86un3 homo sapien
2	141	45.5	420	1	R4RL2_RAT	Q80wd1 rattus norv
3	125	40.3	420	1	R4RL2_MOUSE	Q7m6z0 mus musculu
4	12	3.9	310	2	Q4RRQ4_TETNG	Q4rrq4 tetraodon n
5	12	3.9	324	2	Q4S3K9_TETNG	Q4s3k9 tetraodon n
6	12	3.9	411	2	Q4S6L6_TETNG	Q4s6l6 tetraodon n
7	12	3.9	412	2	Q4RRU8_TETNG	Q4rru8 tetraodon n
8	12	3.9	457	2	Q6WZD1_BRARE	Q6wzdl brachydanio
9	12	3.9	478	2	Q6WZD2_BRARE	Q6wzd2 brachydanio
10	11	3.5	473	1	RTN4R_HUMAN	Q9bzr6 homo sapien
11	11	3.5	473	1	RTN4R_MACFA	Q9n0e3 macaca fasc
12	11	3.5	473	1	RTN4R_MOUSE	Q99pi8 mus musculu
13	11	3.5	473	1	RTN4R_RAT	Q99m75 rattus norv
14	10	3.2	265	2	Q3PEZ7_PARDE	Q3pez7 paracoccus
15	10	3.2	441	1	R4RL1_HUMAN	Q86un2 homo sapien

16	10	3.2	445	1	R4RL1_MOUSE	Q8k0s5 mus musculu
17	10	3.2	445	1	R4RL1_RAT	Q80wd0 rattus norv
18	9	2.9	321	2	Q3MSG3_KLEOX	Q3msg3 klebsiella
19	9	2.9	321	2	Q3MSI6_KLEPN	Q3msi6 klebsiella
20	9	2.9	400	2	Q45WB1_TOXGO	Q45wb1 toxoplasma
21	9	2.9	426	2	Q655P5_ORYSA	Q655p5 oryza sativ
22	9	2.9	458	2	Q6WZD3_BRARE	Q6wzd3 brachydanio
23	9	2.9	479	2	Q6DH76_BRARE	Q6dh76 brachydanio
24	9	2.9	479	2	Q6X3Y5_BRARE	Q6x3y5 brachydanio
25	9	2.9	686	2	Q5FLT7_LACAC	Q5flt7 lactobacill
26	9	2.9	1207	2	Q2JZJ1_RHIET	Q2jzj1 rhizobium e
27	8	2.6	76	2	Q5FE50_EHRRW	Q5fe50 ehrlichia r
28	8	2.6	87	2	Q6J1Q3_9CAUD	Q6j1q3 burkholderi
29	8	2.6	88	2	Q4KIV0_PSEF5	Q4kiv0 pseudomonas
30	8	2.6	93	2	Q3ITV5_NATPD	Q3itv5 natronomona
31	8	2.6	118	2	Q7U642_SYNPX	Q7u642 synechococc
32	8	2.6	119	2	Q6FA35_ACIAD	Q6fa35 acinetobact
33	8	2.6	122	1	INSL3_MOUSE	O09107 mus musculu
34	8	2.6	122	2	Q5RL10_MOUSE	Q5rl10 mus musculu
35	8	2.6	139	2	Q2XGG0_PSEPU	Q2xgg0 pseudomonas
36	8	2.6	139	2	Q9KHT5_PSEPU	Q9kht5 pseudomonas
37	8	2.6	139	2	Q88ME0_PSEPK	Q88me0 pseudomonas
38	8	2.6	149	2	Q3BVP0_XANC5	Q3bvp0 xanthomonas
39	8	2.6	149	2	Q8PMN9_XANAC	Q8pmn9 xanthomonas
40	8	2.6	150	2	Q4HMH8_CAMLA	Q4hmh8 campylobact
41	8	2.6	159	2	Q43Z29_SOLUS	Q43z29 solibacter
42	8	2.6	161	2	Q3P6K2_9GAMM	Q3p6k2 shewanella
43	8	2.6	164	2	Q3X0V7_9ACTN	Q3x0v7 rubrobacter
44	8	2.6	181	1	AROL_SALTI	P63604 salmonella
45	8	2.6	181	1	AROL_SALTY	P63603 salmonella

ALIGNMENTS

RESULT 1

R4RL2_HUMAN

ID R4RL2_HUMAN STANDARD; PRT; 420 AA.
 AC Q86UN3; Q6X813;
 DT 07-FEB-2006, integrated into UniProtKB/Swiss-Prot.
 DT 01-JUN-2003, sequence version 1.
 DT 07-MAR-2006, entry version 18.
 DE Reticulon-4 receptor-like 2 precursor (Nogo-66 receptor homolog 1)
 DE (Nogo-66 receptor-related protein 2) (NgR2) (Nogo receptor-like 3).
 GN Name=RTN4RL2; Synonyms=NGRH1, NGRL3;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [mRNA], SUBCELLULAR LOCATION, AND TISSUE
 RP SPECIFICITY.
 RC TISSUE=Brain;
 RX MEDLINE=22581832; PubMed=12694398;
 RA Pignot V., Hein A.E., Barske C., Wiessner C., Walmsley A.R.,
 RA Kaupmann K., Mayeur H., Sommer B., Mir A.K., Frentzel S.;

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OM protein - protein search, using sw model

Run on: June 20, 2006, 10:08:00 ; Search time 137.627 Seconds
(without alignments)
930.199 Million cell updates/sec

Title: US-10-735-256-2_COPY_31_310
Perfect score: 1477
Sequence: 1 CPMLCTCYSSPPTVSCQANN.....PPERQGRDLRALREADFQAC 280

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_8:
1: geneseqp1980s:
2: geneseqp1990s:
3: geneseqp2000s:
4: geneseqp2001s:
5: geneseqp2002s:
6: geneseqp2003as:
7: geneseqp2003bs:
8: geneseqp2004s:
9: geneseqp2005s:
10: geneseqp2006s:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query					Description
	No.	Score	Match	Length	DB ID	
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1	1477	100.0	390	5	AAO21482	Aao21482 Mature hu
2	1477	100.0	390	7	ADF28529	Adf28529 NgRH _y mat
3	1477	100.0	401	6	AAE33486	Aae33486 Human REM
4	1477	100.0	401	7	ADE07875	Ade07875 Novel pro
5	1477	100.0	401	7	ADF28528	Adf28528 NgRH _y mut
6	1477	100.0	419	8	ADM72131	Adm72131 Human NTR
7	1477	100.0	420	5	AAO21477	Aao21477 Human NgR

8	1477	100.0	420	6	ABR55621	Abr55621 Amino aci
9	1477	100.0	420	7	ADF28510	Adf28510 NgRH _y pre
10	1477	100.0	420	8	ADS10516	Ads10516 Human the
11	1461.5	99.0	512	7	ADC13559	Adc13559 Human NOV
12	1449	98.1	286	8	ADT77787	Adt77787 Rat Nogo
13	1449	98.1	420	6	ABR55628	Abr55628 Amino aci
14	1449	98.1	420	8	ADT77788	Adt77788 Rat Nogo
15	1449	98.1	452	8	ADT77808	Adt77808 Chimeric
16	1449	98.1	452	8	ADT77802	Adt77802 Chimeric
17	1449	98.1	474	8	ADT77796	Adt77796 Chimeric
18	1277.5	86.5	807	4	ABG15173	Abg15173 Novel hum
19	886	60.0	445	8	ADT77794	Adt77794 Rat Nogo
20	885	59.9	415	8	ADT77800	Adt77800 Chimeric
21	885	59.9	441	6	AAO27001	Aao27001 Human NgR
22	885	59.9	441	8	ADN12047	Adn12047 Novel hum
23	885	59.9	445	6	AAO27009	Aao27009 Rat NgRH2
24	885	59.9	445	8	ADN12049	Adn12049 Novel rat
25	885	59.9	445	8	ADT77790	Adt77790 Rat Nogo
26	885	59.9	473	8	ADT77795	Adt77795 Polypepti
27	879	59.5	421	5	AAO21483	Aao21483 Mature mo
28	879	59.5	461	5	AAO21478	Aao21478 Mouse NgR
29	791	53.6	392	5	AAO21487	Aao21487 Partial h
30	775.5	52.5	473	8	ADG75446	Adg75446 Macaque b
31	770.5	52.2	283	6	ABR59685	Abr59685 Human Nog
32	770.5	52.2	285	8	ADU21103	Adu21103 Human Nog
33	770.5	52.2	285	9	AEB19607	Aeb19607 Human sol
34	770.5	52.2	285	9	AEB86599	Aeb86599 Human NOG
35	770.5	52.2	310	8	ADM33975	Adm33975 Human Nog
36	770.5	52.2	310	9	ADY34441	Ady34441 Human Nog
37	770.5	52.2	310	9	AEB19598	Aeb19598 Human Nog
38	770.5	52.2	319	8	ADU21104	Adu21104 Human Nog
39	770.5	52.2	319	9	AEB19606	Aeb19606 Human sol
40	770.5	52.2	319	9	AEB86600	Aeb86600 Human NOG
41	770.5	52.2	344	8	ADM33974	Adm33974 Human Nog
42	770.5	52.2	344	8	ADU21101	Adu21101 Human Nog
43	770.5	52.2	344	9	ADY34440	Ady34440 Human Nog
44	770.5	52.2	344	9	AEB19597	Aeb19597 Human Nog
45	770.5	52.2	344	9	AEB86619	Aeb86619 Human NOG

ALIGNMENTS

RESULT 1

AAO21482

ID AAO21482 standard; protein; 390 AA.

XX

AC AAO21482;

XX

DT 15-AUG-2002 (first entry)

XX

DE Mature human NgR2 protein sequence.

XX

KW Cerebroprotective; neuroprotective; cytostatic; Nogo receptor homologue;

KW NgR2; NgR3; axonal growth; central nervous system; CNS; cerebral injury;

KW spinal cord injury; stroke; demyelinating disease; multiple sclerosis;

KW monophasic demyelination; encephalomyelitis; Marchiafava-Bignami disease;

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OM protein - protein search, using sw model

Run on: June 20, 2006, 10:54:09 ; Search time 34.6441 Seconds
(without alignments)
707.439 Million cell updates/sec

Title: US-10-735-256-2_COPY_31_310
Perfect score: 1477
Sequence: 1 CPMLCTCYSSPPTVSCQANN.....PPERQGRDLRALREADFQAC 280

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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3: /EMC_Celerra_SIDS3/ptodata/2/iaa/7_COMB.pep:
4: /EMC_Celerra_SIDS3/ptodata/2/iaa/H_COMB.pep:
5: /EMC_Celerra_SIDS3/ptodata/2/iaa/PCTUS_COMB.pep:
6: /EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:
7: /EMC_Celerra_SIDS3/ptodata/2/iaa/backfiles1.pep:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query					Description
	No.	Score	Match	Length	DB ID	
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2	770.5	52.2	473	2	US-09-999-833A-400	Sequence 400, App
3	770.5	52.2	473	2	US-10-020-445A-400	Sequence 400, App
4	770.5	52.2	473	2	US-09-978-189-400	Sequence 400, App
5	770.5	52.2	473	2	US-10-017-085A-400	Sequence 400, App
6	770.5	52.2	473	3	US-10-145-129A-400	Sequence 400, App
7	770.5	52.2	473	3	US-10-013-929A-400	Sequence 400, App
8	770.5	52.2	473	3	US-10-013-917A-400	Sequence 400, App
9	767.5	52.0	380	2	US-09-461-325-161	Sequence 161, App
10	767.5	52.0	380	2	US-10-012-542-161	Sequence 161, App

11	767.5	52.0	380	2	US-10-115-123-161	Sequence 161, App
12	355	24.0	481	2	US-09-853-753-2	Sequence 2, Appli
13	355	24.0	485	2	US-09-949-016-8704	Sequence 8704, Ap
14	351	23.8	605	2	US-09-063-950-5	Sequence 5, Appli
15	349	23.6	605	1	US-08-190-802A-49	Sequence 49, Appl
16	349	23.6	605	2	US-08-477-346-49	Sequence 49, Appl
17	349	23.6	605	2	US-08-473-089-49	Sequence 49, Appl
18	349	23.6	605	2	US-08-487-072A-49	Sequence 49, Appl
19	349	23.6	605	2	US-09-538-092-1087	Sequence 1087, Ap
20	349	23.6	623	2	US-09-949-016-10995	Sequence 10995, A
21	337.5	22.9	545	3	US-10-114-270-38	Sequence 38, Appl
22	334.5	22.6	545	3	US-10-114-270-40	Sequence 40, Appl
23	330.5	22.4	498	2	US-10-188-495-51	Sequence 51, Appl
24	330.5	22.4	591	2	US-10-188-495-50	Sequence 50, Appl
25	330.5	22.4	622	2	US-10-188-495-48	Sequence 48, Appl
26	326	22.1	448	2	US-09-520-781-32	Sequence 32, Appl
27	326	22.1	448	2	US-09-957-187-32	Sequence 32, Appl
28	326	22.1	448	2	US-09-991-053-32	Sequence 32, Appl
29	326	22.1	590	2	US-09-520-781-12	Sequence 12, Appl
30	326	22.1	590	2	US-09-957-187-12	Sequence 12, Appl
31	326	22.1	590	2	US-09-991-053-12	Sequence 12, Appl
32	326	22.1	653	2	US-09-520-781-10	Sequence 10, Appl
33	326	22.1	653	2	US-09-957-187-10	Sequence 10, Appl
34	326	22.1	653	2	US-09-991-181-229	Sequence 229, App
35	326	22.1	653	2	US-09-990-444-229	Sequence 229, App
36	326	22.1	653	2	US-09-991-053-10	Sequence 10, Appl
37	326	22.1	653	2	US-09-997-333-229	Sequence 229, App
38	326	22.1	653	2	US-09-992-598-229	Sequence 229, App
39	326	22.1	653	2	US-09-989-735-229	Sequence 229, App
40	326	22.1	653	3	US-09-989-726-229	Sequence 229, App
41	326	22.1	653	3	US-09-997-514-229	Sequence 229, App
42	326	22.1	653	3	US-09-989-728-229	Sequence 229, App
43	326	22.1	653	3	US-09-997-349-229	Sequence 229, App
44	326	22.1	653	3	US-09-997-653-229	Sequence 229, App
45	326	22.1	653	3	US-09-989-293A-229	Sequence 229, App

ALIGNMENTS

RESULT 1

US-09-949-016-8448
; Sequence 8448, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES
THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498

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OM protein - protein search, using sw model

Run on: June 20, 2006, 11:24:49 ; Search time 117.695 Seconds
(without alignments)
1102.003 Million cell updates/sec

Title: US-10-735-256-2_COPY_31_310
Perfect score: 1477
Sequence: 1 CPMLCTCYSSPPTVSCQANN.....PPERQGRDLRALREADFQAC 280

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*

5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*

6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Result No.	Query					Description
	Score	Match	Length	DB	ID	
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1	1477	100.0	390	3	US-09-972-546-8	Sequence 8, Appli
2	1477	100.0	390	5	US-10-735-256-8	Sequence 8, Appli
3	1477	100.0	390	5	US-10-496-905-439	Sequence 439, App
4	1477	100.0	401	5	US-10-477-714-17	Sequence 17, Appli
5	1477	100.0	401	5	US-10-496-905-438	Sequence 438, App
6	1477	100.0	420	3	US-09-972-546-2	Sequence 2, Appli
7	1477	100.0	420	5	US-10-735-256-2	Sequence 2, Appli
8	1477	100.0	420	5	US-10-496-905-420	Sequence 420, App
9	1477	100.0	420	5	US-10-491-810A-2	Sequence 2, Appli
10	1461.5	99.0	512	4	US-10-188-248-38	Sequence 38, Appli
11	1449	98.1	420	5	US-10-491-810A-25	Sequence 25, Appli

12	1277.5	86.5	807	5	US-10-450-763-45532	Sequence 45532, A
13	885	59.9	441	5	US-10-487-886-2	Sequence 2, Appli
14	885	59.9	445	5	US-10-487-886-25	Sequence 25, Appli
15	879	59.5	421	3	US-09-972-546-9	Sequence 9, Appli
16	879	59.5	421	5	US-10-735-256-9	Sequence 9, Appli
17	879	59.5	461	3	US-09-972-546-4	Sequence 4, Appli
18	879	59.5	461	5	US-10-735-256-4	Sequence 4, Appli
19	791	53.6	392	3	US-09-972-546-14	Sequence 14, Appli
20	791	53.6	392	5	US-10-735-256-14	Sequence 14, Appli
21	775.5	52.5	473	4	US-10-271-078-7	Sequence 7, Appli
22	770.5	52.2	283	3	US-09-972-599A-55	Sequence 55, Appli
23	770.5	52.2	310	6	US-11-055-163-7	Sequence 7, Appli
24	770.5	52.2	344	6	US-11-055-163-6	Sequence 6, Appli
25	770.5	52.2	473	3	US-09-758-140-2	Sequence 2, Appli
26	770.5	52.2	473	3	US-09-893-348-26	Sequence 26, Appli
27	770.5	52.2	473	3	US-09-972-599A-2	Sequence 2, Appli
28	770.5	52.2	473	3	US-09-978-295A-400	Sequence 400, App
29	770.5	52.2	473	3	US-09-978-697-400	Sequence 400, App
30	770.5	52.2	473	3	US-09-978-192A-400	Sequence 400, App
31	770.5	52.2	473	3	US-09-999-832A-400	Sequence 400, App
32	770.5	52.2	473	3	US-09-978-189-400	Sequence 400, App
33	770.5	52.2	473	3	US-09-978-608A-400	Sequence 400, App
34	770.5	52.2	473	3	US-09-978-585A-400	Sequence 400, App
35	770.5	52.2	473	3	US-09-978-191A-400	Sequence 400, App
36	770.5	52.2	473	3	US-09-978-403A-400	Sequence 400, App
37	770.5	52.2	473	3	US-09-978-564A-400	Sequence 400, App
38	770.5	52.2	473	3	US-09-999-833A-400	Sequence 400, App
39	770.5	52.2	473	3	US-09-981-915A-400	Sequence 400, App
40	770.5	52.2	473	3	US-09-978-824-400	Sequence 400, App
41	770.5	52.2	473	3	US-09-918-585A-400	Sequence 400, App
42	770.5	52.2	473	3	US-09-999-834A-400	Sequence 400, App
43	770.5	52.2	473	3	US-09-978-423A-400	Sequence 400, App
44	770.5	52.2	473	3	US-09-978-193A-400	Sequence 400, App
45	770.5	52.2	473	3	US-09-999-830A-400	Sequence 400, App

ALIGNMENTS

RESULT 1

US-09-972-546-8
; Sequence 8, Application US/09972546
; Publication No. US20030124704A1
; GENERAL INFORMATION:
; APPLICANT: STRITTMATTER, STEPHEN M.
; APPLICANT: CATE, RICHARD L.
; APPLICANT: SAH, DINAH W.Y.
; TITLE OF INVENTION: NOGO RECEPTOR HOMOLOGS
; FILE REFERENCE: A116US
; CURRENT APPLICATION NUMBER: US/09/972,546
; CURRENT FILING DATE: 2001-10-06
; PRIOR APPLICATION NUMBER: 60/238,361
; PRIOR FILING DATE: 2000-10-06
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 390

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: June 20, 2006, 11:26:34 ; Search time 6.16949 Seconds
(without alignments)
1023.724 Million cell updates/sec

Title: US-10-735-256-2_COPY_31_310
Perfect score: 1477
Sequence: 1 CPMLCTCYSSPPTVSCQANN..... PPERQGRDLRALREADFQAC 280

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 96747 seqs, 22556637 residues

Total number of hits satisfying chosen parameters: 96747

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA_New:
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6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10_NEW_PUB.pep:
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8: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US60_NEW_PUB.pep:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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		Match	Length	DB	
1	333	22.5	811	6	US-10-505-928-32 Sequence 32, Appl
2	333	22.5	811	6	US-10-505-928-87 Sequence 87, Appl
3	325.5	22.0	673	7	US-11-101-316-16 Sequence 16, Appl
4	290	19.6	294	6	US-10-505-928-33 Sequence 33, Appl
5	283.5	19.2	1523	6	US-10-196-749-290 Sequence 290, App
6	272.5	18.4	513	7	US-11-101-316-124 Sequence 124, App
7	269	18.2	370	7	US-11-293-697-3248 Sequence 3248, Ap
8	259	17.5	598	7	US-11-296-092-69 Sequence 69, Appl
9	258.5	17.5	649	6	US-10-196-749-384 Sequence 384, App

10	258.5	17.5	649	7	US-11-101-316-132	Sequence 132, App
11	258	17.5	716	6	US-10-518-039-6	Sequence 6, Appli
12	258	17.5	812	6	US-10-518-039-5	Sequence 5, Appli
13	239	16.2	359	6	US-10-933-854-18	Sequence 18, Appl
14	238	16.1	719	7	US-11-293-697-3841	Sequence 3841, Ap
15	224.5	15.2	611	6	US-10-520-783-2	Sequence 2, Appli
16	222	15.0	745	7	US-11-293-697-3826	Sequence 3826, Ap
17	219.5	14.9	557	6	US-10-196-749-326	Sequence 326, App
18	211.5	14.3	379	7	US-11-296-092-2	Sequence 2, Appli
19	203	13.7	290	7	US-11-257-581-10	Sequence 10, Appli
20	203	13.7	302	7	US-11-257-581-7	Sequence 7, Appli
21	203	13.7	302	7	US-11-257-581-8	Sequence 8, Appli
22	203	13.7	531	7	US-11-257-581-4	Sequence 4, Appli
23	203	13.7	544	7	US-11-257-581-1	Sequence 1, Appli
24	203	13.7	544	7	US-11-257-581-2	Sequence 2, Appli
25	202.5	13.7	290	7	US-11-257-581-11	Sequence 11, Appli
26	202.5	13.7	290	7	US-11-257-581-12	Sequence 12, Appli
27	202.5	13.7	301	7	US-11-257-581-9	Sequence 9, Appli
28	202.5	13.7	531	7	US-11-257-581-5	Sequence 5, Appli
29	202.5	13.7	531	7	US-11-257-581-6	Sequence 6, Appli
30	202.5	13.7	544	7	US-11-257-581-3	Sequence 3, Appli
31	199.5	13.5	368	6	US-10-505-928-743	Sequence 743, App
32	189.5	12.8	703	7	US-11-291-140-4	Sequence 4, Appli
33	189.5	12.8	904	7	US-11-144-322-2	Sequence 2, Appli
34	189.5	12.8	904	7	US-11-291-140-2	Sequence 2, Appli
35	183	12.4	977	6	US-10-449-902-50526	Sequence 50526, A
36	180.5	12.2	692	6	US-10-196-749-560	Sequence 560, App
37	178.5	12.1	616	6	US-10-196-749-158	Sequence 158, App
38	178.5	12.1	1032	6	US-10-196-749-552	Sequence 552, App
39	171.5	11.6	1123	6	US-10-953-349-4749	Sequence 4749, Ap
40	169	11.4	1135	6	US-10-449-902-56546	Sequence 56546, A
41	168.5	11.4	501	6	US-10-449-902-48020	Sequence 48020, A
42	168	11.4	964	6	US-10-449-902-47345	Sequence 47345, A
43	167	11.3	546	6	US-10-196-749-412	Sequence 412, App
44	166.5	11.3	293	6	US-10-953-349-22365	Sequence 22365, A
45	166.5	11.3	598	6	US-10-953-349-7417	Sequence 7417, Ap

ALIGNMENTS

RESULT 1

US-10-505-928-32
; Sequence 32, Application US/10505928
; Publication No. US20060088532A1
; GENERAL INFORMATION:
; APPLICANT: Ludwig Institute for Cancer Research et al.
; TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
; FILE REFERENCE: 28967/39178
; CURRENT APPLICATION NUMBER: US/10/505,928
; CURRENT FILING DATE: 2004-08-27
; PRIOR APPLICATION NUMBER: US 60/363,019
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 866
; SOFTWARE: PatentIn 3.2
; SEQ ID NO 32
; LENGTH: 811

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OM protein - protein search, using sw model

Run on: June 20, 2006, 10:51:54 ; Search time 12.8136 Seconds
(without alignments)
2102.514 Million cell updates/sec

Title: US-10-735-256-2_COPY_31_310
Perfect score: 1477
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_80:*

1: pirl:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query					Description
No.	Score	Match	Length	DB	ID	Description
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2	349	23.6	605	2	A41915	insulin-like growth factor binding protein 1
3	330.5	22.4	622	2	JC7973	synleucin - human
4	324.5	22.0	1469	2	B36665	slit protein 2 pre-mRNA
5	324.5	22.0	1480	2	A36665	slit protein 1 pre-mRNA
6	324	21.9	603	2	JC1282	insulin-like growth factor binding protein 1
7	321	21.7	603	2	JC6128	insulin-like growth factor binding protein 1
8	319	21.6	420	2	A53531	oncofetal trophoblast protein
9	308	20.9	361	2	A53860	chondroadherin pre-mRNA
10	297.5	20.1	1531	2	T42218	slit-1 protein homolog
11	297	20.1	560	2	A60164	platelet membrane protein
12	280.5	19.0	312	1	NBHUA2	leucine-rich alpha-2-macroglobulin
13	279.5	18.9	1523	2	T13953	MEGF5 protein - rat

14	278	18.8	707	2	JC7763	neuronal leucine-r
15	278	18.8	1091	2	A58532	glial cell membran
16	273.5	18.5	536	2	A34901	lysine carboxypept
17	255.5	17.3	360	2	S06280	decorin precursor
18	249.5	16.9	907	2	JE0176	orphan G protein-c
19	242.5	16.4	1535	2	S46224	peroxidasin - frui
20	240	16.2	789	2	T28714	hypothetical prote
21	240	16.2	1355	2	T28715	hypothetical prote
22	239	16.2	359	1	NBHUC8	decorin precursor
23	239	16.2	360	2	I47020	decorin - rabbit
24	236.5	16.0	354	2	S29145	decorin precursor
25	236.5	16.0	907	2	JG0193	G protein-coupled
26	235.5	15.9	1025	2	T42626	secreted leucine-r
27	234.5	15.9	357	2	S24317	decorin precursor
28	231.5	15.7	382	2	I39068	proline- arginine-
29	231.5	15.7	1112	2	T10504	disease resistance
30	231.5	15.7	1389	2	T13852	gene wheeler prote
31	228.5	15.5	1385	2	T13887	tlr protein - frui
32	227	15.4	662	2	S42799	garp precursor - h
33	227	15.4	682	2	A49121	cell-surface molec
34	227	15.4	682	2	A43318	connectin precurs
35	226.5	15.3	354	2	A55454	decorin precursor
36	222	15.0	562	2	T34319	hypothetical prote
37	220	14.9	594	2	T23841	hypothetical prote
38	220	14.9	610	2	T23836	hypothetical prote
39	217.5	14.7	738	2	T19938	hypothetical prote
40	211	14.3	1016	2	T30553	disease resistance
41	205.5	13.9	1066	2	T15864	hypothetical prote
42	204	13.8	1134	1	A29944	chaoptin precursor
43	203	13.7	626	1	NBHUIA	platelet glycoprot
44	199.5	13.5	368	1	BGHUN	biglycan precursor
45	199	13.5	375	2	S05390	fibromodulin precu

ALIGNMENTS

RESULT 1
JC5239
insulin-like growth factor acid-labile chain - baboon
C;Species: Papio sp. (baboon)
C;Date: 17-Apr-1997 #sequence_revision 09-May-1997 #text_change 09-May-1997
C;Accession: JC5239
R;Delhanty, P.; Baxter, R.C.
Biochem. Biophys. Res. Commun. 227, 897-902, 1996
A;Title: The cloning and expression of the baboon acid-labile subunit of the insulin-like growth factor binding protein complex.
A;Reference number: JC5239; MUID:97040714; PMID:8886027
A;Contents: liver
A;Accession: JC5239
A;Molecule type: mRNA
A;Residues: 1-605
A;Cross-references: UNIPARC:UPI000000D50E
C;Comment: This factor is structurally related to proinsulin and have insuline-like metabolic, differentiative, and cell proliferative activities.

Query Match 23.8%; Score 351; DB 2; Length 605;

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OM protein - protein search, using sw model

Run on: June 20, 2006, 10:13:29 ; Search time 182.712 Seconds
(without alignments)
1417.556 Million cell updates/sec

Title: US-10-735-256-2_COPY_31_310
Perfect score: 1477
Sequence: 1 CPMLCTCYSSPPTVSCQANN.....PPERQGRDLRALREADFQAC 280

Scoring table: BLOSUM62
Gapext 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_7.2:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query					Description
No.	Score	Match	Length	DB	ID	
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1	1477	100.0	420	1	R4RL2_HUMAN	Q86un3 homo sapien
2	1449	98.1	420	1	R4RL2_MOUSE	Q7m6z0 mus musculu
3	1449	98.1	420	1	R4RL2_RAT	Q80wd1 rattus norv
4	935	63.3	411	2	Q4S6L6_TETNG	Q4s6l6 tetraodon n
5	923	62.5	457	2	Q6WZD1_BRARE	Q6wzd1 brachydanio
6	914	61.9	458	2	Q6WZD3_BRARE	Q6wzd3 brachydanio
7	906	61.3	478	2	Q6WZD2_BRARE	Q6wzd2 brachydanio
8	902.5	61.1	324	2	Q4S3K9_TETNG	Q4s3k9 tetraodon n
9	893	60.5	310	2	Q4RRQ4_TETNG	Q4rrq4 tetraodon n
10	885	59.9	441	1	R4RL1_HUMAN	Q86un2 homo sapien
11	885	59.9	445	1	R4RL1_RAT	Q80wd0 rattus norv
12	879	59.5	445	1	R4RL1_MOUSE	Q8k0s5 mus musculu
13	850	57.5	412	2	Q4RRU8_TETNG	Q4rru8 tetraodon n
14	797.5	54.0	479	2	Q6DH76_BRARE	Q6dh76 brachydanio
15	797.5	54.0	479	2	Q6X3Y5_BRARE	Q6x3y5 brachydanio

16	775.5	52.5	473	1	RTN4R_MACFA	Q9n0e3 macaca fasc
17	770.5	52.2	473	1	RTN4R_HUMAN	Q9bzr6 homo sapien
18	754.5	51.1	473	1	RTN4R_RAT	Q99m75 rattus norv
19	740.5	50.1	473	1	RTN4R_MOUSE	Q99pi8 mus musculu
20	377.5	25.6	417	2	Q6E4J7_PETMA	Q6e4j7 petromyzon
21	365	24.7	290	2	Q2VGX3_PETMA	Q2vgx3 petromyzon
22	361.5	24.5	411	2	Q4S9P3_TETNG	Q4s9p3 tetraodon n
23	359.5	24.3	578	1	LRC15_RAT	Q8r5m3 rattus norv
24	355	24.0	481	1	NYX_HUMAN	Q9gzu5 homo sapien
25	355	24.0	481	2	Q2M1S4_HUMAN	Q2mls4 homo sapien
26	355	24.0	637	2	Q6DCV7_XENLA	Q6dcv7 xenopus lae
27	352.5	23.9	264	2	Q2VGT2_PETMA	Q2vgt2 petromyzon
28	352.5	23.9	339	2	Q4SU68_TETNG	Q4su68 tetraodon n
29	351.5	23.8	579	1	LRC15_MOUSE	Q80x72 mus musculu
30	351	23.8	513	2	Q50LG9_HUMAN	Q50lg9 homo sapien
31	351	23.8	605	1	ALS_PAPHA	O02833 papio hamad
32	350	23.7	605	2	Q8TAY0_HUMAN	Q8tay0 homo sapien
33	350	23.7	692	2	Q4G0S0_HUMAN	Q4g0s0 homo sapien
34	350	23.7	762	2	Q5JY13_HUMAN	Q5jy13 homo sapien
35	350	23.7	778	2	Q6NU16_HUMAN	Q6nu16 homo sapien
36	349	23.6	605	1	ALS_HUMAN	P35858 homo sapien
37	348	23.6	521	2	Q8BHA1_MOUSE	Q8bhal m 0 day neo
38	344.5	23.3	466	2	Q66IW3_XENLA	Q66iw3 xenopus lae
39	344	23.3	393	2	Q32R29_EPTBU	Q32r29 eptatretus
40	342	23.2	476	1	NYX_MOUSE	P83503 mus musculu
41	340	23.0	428	2	Q4S4W6_TETNG	Q4s4w6 tetraodon n
42	337.5	22.9	264	2	Q2VGV6_PETMA	Q2vgv6 petromyzon
43	337.5	22.9	545	1	CPN2_HUMAN	P22792 homo sapien
44	334	22.6	487	2	Q4SA13_TETNG	Q4sa13 tetraodon n
45	333	22.5	811	2	Q7L0X0_HUMAN	Q7l0x0 homo sapien

ALIGNMENTS

RESULT 1

R4RL2_HUMAN

ID R4RL2_HUMAN STANDARD; PRT; 420 AA.
AC Q86UN3; Q6X813;
DT 07-FEB-2006, integrated into UniProtKB/Swiss-Prot.
DT 01-JUN-2003, sequence version 1.
DT 07-MAR-2006, entry version 18.
DE Reticulon-4 receptor-like 2 precursor (Nogo-66 receptor homolog 1)
DE (Nogo-66 receptor-related protein 2) (NgR2) (Nogo receptor-like 3).
GN Name=RTN4RL2; Synonyms=NGRH1, NGRL3;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE [MRNA], SUBCELLULAR LOCATION, AND TISSUE
RP SPECIFICITY.
RC TISSUE=Brain;
RX MEDLINE=22581832; PubMed=12694398;
RA Pignot V., Hein A.E., Barske C., Wiessner C., Walmsley A.R.,
RA Kaupmann K., Mayeur H., Sommer B., Mir A.K., Frentzel S.;

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OM protein - protein search, using sw model

Run on: June 20, 2006, 11:43:57 ; Search time 229.695 Seconds
(without alignments)
557.351 Million cell updates/sec

Title: US-10-735-256-2_COPY_31_310
Perfect score: 280
Sequence: 1 CPMLCTCYSSPPTVSCQANN.....PPEROGRDLRALREADFQAC 280

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 2589679 seqs, 457216429 residues

Word size : 1

Total number of hits satisfying chosen parameters: 2588894

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : A_Geneseq_8:*

1: geneseqp1980s:*

2: geneseqp1990s:*

3: geneseqp2000s:*

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5: geneseqp2002s:*

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8: geneseqp2004s:*

9: geneseqp2005s:*

10: geneseqp2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Result	Query					
No.	Score	Match	Length	DB	ID	Description

1	280	100.0	390	5	AAO21482	Aao21482 Mature hu
2	280	100.0	390	7	ADF28529	Adf28529 NgRH _y mat
3	280	100.0	401	6	AAE33486	Aae33486 Human REM
4	280	100.0	401	7	ADE07875	Ade07875 Novel pro
5	280	100.0	401	7	ADF28528	Adf28528 NgRH _y mut
6	280	100.0	419	8	ADM72131	Adm72131 Human NTR
7	280	100.0	420	5	AAO21477	Aao21477 Human NgR

8	280	100.0	420	6	ABR55621	Abr55621 Amino aci
9	280	100.0	420	7	ADF28510	Adf28510 NgRH _y pre
10	280	100.0	420	8	ADS10516	Ads10516 Human the
11	141	50.4	286	8	ADT77787	Adt77787 Rat Nogo
12	141	50.4	420	6	ABR55628	Abr55628 Amino aci
13	141	50.4	420	8	ADT77788	Adt77788 Rat Nogo
14	141	50.4	452	8	ADT77808	Adt77808 Chimeric
15	141	50.4	452	8	ADT77802	Adt77802 Chimeric
16	141	50.4	474	8	ADT77796	Adt77796 Chimeric
17	140	50.0	512	7	ADC13559	Adc13559 Human NOV
18	133	47.5	241	4	ABG15171	Abg15171 Novel hum
19	126	45.0	807	4	ABG15173	Abg15173 Novel hum
20	50	17.9	51	7	ADF28526	Adf28526 Leucine-r
21	45	16.1	56	4	AAM23826	Aam23826 Human EST
22	45	16.1	56	7	ADE08958	Ade08958 Novel pro
23	45	16.1	56	8	ADS11791	Ads11791 Human the
24	33	11.8	492	4	ABG15172	Abg15172 Novel hum
25	25	8.9	25	7	ADF28520	Adf28520 Leucine-r
26	24	8.6	24	7	ADF28524	Adf28524 Leucine-r
27	24	8.6	24	7	ADF28525	Adf28525 Leucine-r
28	24	8.6	24	7	ADF28523	Adf28523 Leucine-r
29	24	8.6	24	7	ADF28522	Adf28522 Leucine-r
30	24	8.6	24	7	ADF28519	Adf28519 Leucine-r
31	24	8.6	24	7	ADF28521	Adf28521 Leucine-r
32	22	7.9	22	7	ADF28518	Adf28518 Leucine-r
33	15	5.4	15	7	ADF28513	Adf28513 PR00019A
34	15	5.4	15	7	ADF28515	Adf28515 PR00019A
35	15	5.4	15	7	ADF28516	Adf28516 PR00019B
36	15	5.4	15	7	ADF28514	Adf28514 PR00019B
37	15	5.4	15	7	ADF28517	Adf28517 PR00019B
38	14	5.0	114	2	AAY10843	Aay10843 Amino aci
39	14	5.0	114	7	ADB47833	Adb47833 Novel hum
40	14	5.0	114	8	ADJ55388	Adj55388 Novel hum
41	14	5.0	114	9	AED67371	Aed67371 Human imm
42	11	3.9	11	8	ADT77816	Adt77816 Rat Nogo
43	11	3.9	49	6	ABR62021	Abr62021 Mouse Nog
44	11	3.9	49	6	ABR62022	Abr62022 Rat Nogo
45	11	3.9	49	6	ABR62020	Abr62020 Human Nog

ALIGNMENTS

RESULT 1

AAO21482

ID AAO21482 standard; protein; 390 AA.

XX

AC AAO21482;

XX

DT 15-AUG-2002 (first entry)

XX

DE Mature human NgR2 protein sequence.

XX

KW Cerebroprotective; neuroprotective; cytostatic; Nogo receptor homologue;
 KW NgR2; NgR3; axonal growth; central nervous system; CNS; cerebral injury;
 KW spinal cord injury; stroke; demyelinating disease; multiple sclerosis;
 KW monophasic demyelination; encephalomyelitis; Marchiafava-Bignami disease;

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: June 20, 2006, 11:59:16 ; Search time 33.6949 Seconds
(without alignments)
727.367 Million cell updates/sec

Title: US-10-735-256-2_COPY_31_310
Perfect score: 280
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Searched: 650591 seqs, 87530628 residues

Word size : 1

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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5: /EMC_Celerra_SIDS3/ptodata/2/iaa/PCTUS_COMB.pep:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	14	5.0	115	2	US-09-774-639-154 Sequence 154, App
2	11	3.9	380	2	US-09-461-325-161 Sequence 161, App
3	11	3.9	380	.2	US-10-012-542-161 Sequence 161, App
4	11	3.9	380	2	US-10-115-123-161 Sequence 161, App
5	11	3.9	473	2	US-09-949-016-8448 Sequence 8448, Ap
6	11	3.9	473	2	US-09-999-833A-400 Sequence 400, App
7	11	3.9	473	2	US-10-020-445A-400 Sequence 400, App
8	11	3.9	473	2	US-09-978-189-400 Sequence 400, App
9	11	3.9	473	2	US-10-017-085A-400 Sequence 400, App
10	11	3.9	473	3	US-10-145-129A-400 Sequence 400, App

11	11	3.9	473	3	US-10-013-929A-400	Sequence 400, App
12	11	3.9	473	3	US-10-013-917A-400	Sequence 400, App
13	8	2.9	226	2	US-09-489-039A-10549	Sequence 10549, A
14	8	2.9	320	2	US-09-248-796A-16573	Sequence 16573, A
15	8	2.9	446	2	US-09-252-991A-23809	Sequence 23809, A
16	8	2.9	455	2	US-09-793-998-8	Sequence 8, Appli
17	8	2.9	799	3	US-09-396-985B-4	Sequence 4, Appli
18	8	2.9	839	3	US-09-396-985B-2	Sequence 2, Appli
19	8	2.9	839	3	US-09-396-985B-98	Sequence 98, Appli
20	8	2.9	844	2	US-09-949-016-9438	Sequence 9438, Ap
21	8	2.9	990	2	US-10-101-464A-814	Sequence 814, App
22	7	2.5	70	2	US-09-107-532A-4266	Sequence 4266, Ap
23	7	2.5	150	2	US-09-270-767-34661	Sequence 34661, A
24	7	2.5	150	2	US-09-270-767-49878	Sequence 49878, A
25	7	2.5	185	2	US-10-101-464A-519	Sequence 519, App
26	7	2.5	213	2	US-09-328-352-6050	Sequence 6050, Ap
27	7	2.5	222	2	US-09-248-796A-15754	Sequence 15754, A
28	7	2.5	260	2	US-09-902-540-10767	Sequence 10767, A
29	7	2.5	268	2	US-10-104-047-3172	Sequence 3172, Ap
30	7	2.5	269	2	US-09-252-991A-20218	Sequence 20218, A
31	7	2.5	270	2	US-09-252-991A-22477	Sequence 22477, A
32	7	2.5	271	2	US-09-902-540-11216	Sequence 11216, A
33	7	2.5	283	2	US-09-252-991A-27181	Sequence 27181, A
34	7	2.5	291	2	US-09-134-001C-3893	Sequence 3893, Ap
35	7	2.5	310	2	US-10-094-749-3057	Sequence 3057, Ap
36	7	2.5	320	2	US-09-325-932A-190	Sequence 190, App
37	7	2.5	322	2	US-10-101-464A-648	Sequence 648, App
38	7	2.5	326	2	US-09-252-991A-18751	Sequence 18751, A
39	7	2.5	354	2	US-09-067-089-2	Sequence 2, Appli
40	7	2.5	354	2	US-09-574-377-32	Sequence 32, Appl
41	7	2.5	354	2	US-09-574-377-33	Sequence 33, Appl
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ALIGNMENTS

RESULT 1

US-09-774-639-154

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; Sequence 154, Application US/09774639
; Patent No. 6806351
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 90 Human Secreted Proteins
; FILE REFERENCE: PZ013P1
; CURRENT APPLICATION NUMBER: US/09/774,639
; CURRENT FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/244,112
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-02-04
; NUMBER OF SEQ ID NOS: 371
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 154
; LENGTH: 115
; TYPE: PRT
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OM protein - protein search, using sw model

Run on: June 20, 2006, 12:15:51 ; Search time 116.746 Seconds
(without alignments)
1110.962 Million cell updates/sec

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Gapop 60.0 , Gapext 60.0

Searched: 2097797 seqs, 463214858 residues

Word size : 1

Total number of hits satisfying chosen parameters: 2096261

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	280	100.0	390	5	US-10-496-905-439 Sequence 439, App
4	280	100.0	401	5	US-10-477-714-17 Sequence 17, Appli
5	280	100.0	401	5	US-10-496-905-438 Sequence 438, App
6	280	100.0	420	3	US-09-972-546-2 Sequence 2, Appli
7	280	100.0	420	5	US-10-735-256-2 Sequence 2, Appli
8	280	100.0	420	5	US-10-496-905-420 Sequence 420, App
9	280	100.0	420	5	US-10-491-810A-2 Sequence 2, Appli
10	141	50.4	420	5	US-10-491-810A-25 Sequence 25, Appli
11	140	50.0	512	4	US-10-188-248-38 Sequence 38, Appli

12	133	47.5	241	5	US-10-450-763-45530	Sequence 45530, A
13	126	45.0	807	5	US-10-450-763-45532	Sequence 45532, A
14	50	17.9	51	5	US-10-496-905-436	Sequence 436, App
15	33	11.8	492	5	US-10-450-763-45531	Sequence 45531, A
16	25	8.9	25	5	US-10-496-905-430	Sequence 430, App
17	24	8.6	24	5	US-10-496-905-429	Sequence 429, App
18	24	8.6	24	5	US-10-496-905-431	Sequence 431, App
19	24	8.6	24	5	US-10-496-905-432	Sequence 432, App
20	24	8.6	24	5	US-10-496-905-433	Sequence 433, App
21	24	8.6	24	5	US-10-496-905-434	Sequence 434, App
22	24	8.6	24	5	US-10-496-905-435	Sequence 435, App
23	22	7.9	22	5	US-10-496-905-428	Sequence 428, App
24	15	5.4	15	5	US-10-496-905-423	Sequence 423, App
25	15	5.4	15	5	US-10-496-905-424	Sequence 424, App
26	15	5.4	15	5	US-10-496-905-425	Sequence 425, App
27	15	5.4	15	5	US-10-496-905-426	Sequence 426, App
28	15	5.4	15	5	US-10-496-905-427	Sequence 427, App
29	14	5.0	114	3	US-09-969-730-116	Sequence 116, App
30	14	5.0	114	4	US-10-621-363-116	Sequence 116, App
31	14	5.0	114	5	US-10-986-501-116	Sequence 116, App
32	14	5.0	115	3	US-09-774-639-154	Sequence 154, App
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34	11	3.9	49	4	US-10-006-002-2	Sequence 2, Appli
35	11	3.9	49	4	US-10-006-002-3	Sequence 3, Appli
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37	11	3.9	49	4	US-10-127-058-2	Sequence 2, Appli
38	11	3.9	49	4	US-10-127-058-3	Sequence 3, Appli
39	11	3.9	283	3	US-09-972-599A-55	Sequence 55, Appli
40	11	3.9	310	6	US-11-055-163-7	Sequence 7, Appli
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42	11	3.9	344	6	US-11-055-163-6	Sequence 6, Appli
43	11	3.9	344	6	US-11-055-163-8	Sequence 8, Appli
44	11	3.9	380	4	US-10-012-542-161	Sequence 161, App
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ALIGNMENTS

RESULT 1
 US-09-972-546-8
; Sequence 8, Application US/09972546
; Publication No. US20030124704A1
; GENERAL INFORMATION:
; APPLICANT: STRITTMATTER, STEPHEN M.
; APPLICANT: CATE, RICHARD L.
; APPLICANT: SAH, DINAH W.Y.
; TITLE OF INVENTION: NOGO RECEPTOR HOMOLOGS
; FILE REFERENCE: A116US
; CURRENT APPLICATION NUMBER: US/09/972,546
; CURRENT FILING DATE: 2001-10-06
; PRIOR APPLICATION NUMBER: 60/238,361
; PRIOR FILING DATE: 2000-10-06
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 390

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OM protein - protein search, using sw model

Run on: June 20, 2006, 12:16:16 ; Search time 12.339 Seconds
(without alignments)
511.862 Million cell updates/sec

Title: US-10-735-256-2_COPY_31_310
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Word size : 1

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	7	2.5	278	6	US-10-953-349-4307 Sequence 4307, Ap
4	7	2.5	306	6	US-10-953-349-4306 Sequence 4306, Ap
5	7	2.5	319	6	US-10-449-902-45409 Sequence 45409, A
6	7	2.5	330	6	US-10-953-349-5740 Sequence 5740, Ap
7	7	2.5	332	6	US-10-953-349-5739 Sequence 5739, Ap
8	7	2.5	358	6	US-10-449-902-34744 Sequence 34744, A
9	7	2.5	503	6	US-10-953-349-26067 Sequence 26067, A

10	7	2.5	587	7	US-11-293-697-4811	Sequence 4811, Ap
11	7	2.5	596	6	US-10-449-902-45371	Sequence 45371, A
12	7	2.5	621	7	US-11-106-014-56	Sequence 56, Appl
13	7	2.5	719	7	US-11-293-697-3841	Sequence 3841, Ap
14	7	2.5	1043	7	US-11-293-697-3097	Sequence 3097, Ap
15	6	2.1	11	7	US-11-122-986-354	Sequence 354, App
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17	6	2.1	44	7	US-11-299-304-100	Sequence 100, App
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ALIGNMENTS

RESULT 1

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; Sequence 34272, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870

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OM protein - protein search, using sw model

Run on: June 20, 2006, 11:52:46 ; Search time 24.2034 Seconds
(without alignments)
1113.096 Million cell updates/sec

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Gapop 60.0 , Gapext 60.0

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Word size : 1

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

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3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Result No.	Query Score	Match	Length	DB	ID	Description
1	8	2.9	181	2	AC0550	shikimate kinase I
2	8	2.9	244	2	JC8019	CD58 protein - pig
3	8	2.9	262	1	B64154	probable radical-f
4	8	2.9	481	2	T33733	hypothetical prote
5	8	2.9	925	2	H96638	protein T1F9.20 [i
6	8	2.9	967	2	G96637	hypothetical prote
7	8	2.9	1148	2	D85360	hypothetical prote
8	7	2.5	60	2	AD2255	hypothetical prote
9	7	2.5	62	2	T28346	ORF MSV185 hypothe
10	7	2.5	83	2	D70639	hypothetical prote
11	7	2.5	132	1	B64104	virulence-associat
12	7	2.5	147	1	HBLUA	hemoglobin beta ch
13	7	2.5	154	2	T07767	disease resistance

14	7	2.5	154	2	T07769	disease resistance
15	7	2.5	157	2	G84292	hypothetical prote
16	7	2.5	164	2	T51261	hypothetical prote
17	7	2.5	212	2	B75156	resolvase related
18	7	2.5	216	2	T37221	hypothetical prote
19	7	2.5	219	2	F83160	two-component resp
20	7	2.5	223	2	E83596	DNA mismatch repai
21	7	2.5	225	2	T11279	H+-transporting tw
22	7	2.5	237	2	T26765	hypothetical prote
23	7	2.5	250	2	S75302	hypothetical prote
24	7	2.5	252	2	T01787	thyrotropin recept
25	7	2.5	253	1	JC1319	thyrotropin recept
26	7	2.5	253	2	T00290	psiA protein - Esc
27	7	2.5	260	2	T18554	integral membrane
28	7	2.5	264	2	G83245	probable ATP-bindi
29	7	2.5	283	2	E83053	dihydropteroate sy
30	7	2.5	285	2	A40657	hypothetical prote
31	7	2.5	310	2	T44912	cysteine synthase
32	7	2.5	320	2	T47882	hypothetical prote
33	7	2.5	326	2	D84088	cytosine-specific
34	7	2.5	326	2	C82200	cytochrome c oxida
35	7	2.5	329	2	T17033	leucine rich repea
36	7	2.5	332	2	T47703	Ca-dependent solut
37	7	2.5	343	2	D83839	glucose-resistance
38	7	2.5	351	2	F64880	ycjS protein - Esc
39	7	2.5	356	1	A54038	phenylalanine dehy
40	7	2.5	360	2	C84243	asparagine synthet
41	7	2.5	365	2	F87552	dprA protein [impo
42	7	2.5	383	2	AH2516	hypothetical prote
43	7	2.5	390	2	T35509	hypothetical prote
44	7	2.5	403	2	S58345	E2F-1 transcriptio
45	7	2.5	420	2	T50585	probable membrane

ALIGNMENTS

RESULT 1

AC0550

shikimate kinase II [imported] - *Salmonella enterica* subsp. *enterica* serovar Typhi (strain CT18)

C;Species: *Salmonella enterica* subsp. *enterica* serovar Typhi

A;Note: this species has also been called *Salmonella typhi*

C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002

C;Accession: AC0550

R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, C.; Mungall, K.L.; Bentley, S.D.; Holden, M.T.G.; Sebaihia, M.; Baker, S.; Basham, D.; Brooks, K.; Chillingworth, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, J.; Feltwell, T.; Hamlin, N.; Haque, A.; Hien, T.T.; Holroyd, S.; Jagels, K.; Krogh, A.; Larsen, T.S.; Leather, S.; Moule, S.; O'Gaora, P.

Nature 413, 848-852, 2001

A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, B.G.

A;Title: Complete genome sequence of a multiple drug resistant *Salmonella enterica* serovar Typhi CT18.

A;Reference number: AB0502; MUID:21534947; PMID:11677608

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: June 20, 2006, 11:44:20 ; Search time 182.237 Seconds
(without alignments)
1421.248 Million cell updates/sec

Title: US-10-735-256-2_COPY_31_310
Perfect score: 280
Sequence: 1 CPMLCTCYSSPPTVSCQANN.....PPERQGRDLRALREADFQAC 280

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 2849598 seqs, 925015592 residues

Word size : 1

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : UniProt_7.2:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query					Description
No.	Score	Match	Length	DB	ID	
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1	280	100.0	420	1	R4RL2_HUMAN	Q86un3 homo sapien
2	141	50.4	420	1	R4RL2_RAT	Q80wd1 rattus norv
3	125	44.6	420	1	R4RL2_MOUSE	Q7m6z0 mus musculu
4	12	4.3	310	2	Q4RRQ4_TETNG	Q4rrq4 tetraodon n
5	12	4.3	324	2	Q4S3K9_TETNG	Q4s3k9 tetraodon n
6	12	4.3	411	2	Q4S6L6_TETNG	Q4s6l6 tetraodon n
7	12	4.3	412	2	Q4RRU8_TETNG	Q4rru8 tetraodon n
8	12	4.3	457	2	Q6WZD1_BRARE	Q6wzdl brachydanio
9	12	4.3	478	2	Q6WZD2_BRARE	Q6wzd2 brachydanio
10	11	3.9	473	1	RTN4R_HUMAN	Q9bzr6 homo sapien
11	11	3.9	473	1	RTN4R_MACFA	Q9n0e3 macaca fasc
12	11	3.9	473	1	RTN4R_MOUSE	Q99pi8 mus musculu
13	11	3.9	473	1	RTN4R_RAT	Q99m75 rattus norv
14	10	3.6	441	1	R4RL1_HUMAN	Q86un2 homo sapien
15	10	3.6	445	1	R4RL1_MOUSE	Q8k0s5 mus musculu

16	10	3.6	445	1	R4RL1_RAT	Q80wd0 rattus norv
17	9	3.2	321	2	Q3MSG3_KLEOX	Q3msg3 klebsiella
18	9	3.2	321	2	Q3MSI16_KLEPN	Q3msi6 klebsiella
19	9	3.2	400	2	Q45WB1_TOXGO	Q45wb1 toxoplasma
20	9	3.2	458	2	Q6WZD3_BRARE	Q6wzd3 brachydanio
21	9	3.2	479	2	Q6DH76_BRARE	Q6dh76 brachydanio
22	9	3.2	479	2	Q6X3Y5_BRARE	Q6x3y5 brachydanio
23	9	3.2	686	2	Q5FLT7_LACAC	Q5flt7 lactobacill
24	9	3.2	1207	2	Q2JZJ1_RHIET	Q2jzj1 rhizobium e
25	8	2.9	93	2	Q3ITV5_NATPD	Q3itv5 natronomona
26	8	2.9	150	2	Q4HMH8_CAMLA	Q4hmh8 campylobact
27	8	2.9	161	2	Q3P6K2_9GAMM	Q3p6k2 shewanella
28	8	2.9	181	1	AROL_SALTI	P63604 salmonella
29	8	2.9	181	1	AROL_SALTY	P63603 salmonella
30	8	2.9	181	2	Q57SH6_SALCH	Q57sh6 salmonella
31	8	2.9	181	2	Q5PFV5_SALPA	Q5pfv5 salmonella
32	8	2.9	197	2	Q4IYH4_AZOVI	Q4iyh4 azotobacter
33	8	2.9	210	1	KGUA_IDILO	Q5qyh9 idiomarina
34	8	2.9	216	2	Q5SKH3_THET8	Q5skh3 thermus the
35	8	2.9	219	2	Q7FAK9_ORYSA	Q7fak9 oryza sativ
36	8	2.9	228	2	Q8SAS9_SOYBN	Q8sas9 glycine max
37	8	2.9	241	2	Q5UCB1_TRYCR	Q5ucb1 trypanosoma
38	8	2.9	244	2	Q7YS40_PIG	Q7ys40 sus scrofa
39	8	2.9	244	2	Q8SQB6_PIG	Q8sqb6 sus scrofa
40	8	2.9	246	2	Q72KM2_THET2	Q72km2 thermus the
41	8	2.9	262	1	Y520_HAEIN	P44743 haemophilus
42	8	2.9	262	2	Q4QN28_HAEI8	Q4qn28 haemophilus
43	8	2.9	280	2	Q2RVY3_RHORU	Q2rvy3 rhodospiril
44	8	2.9	280	2	Q4BSV7_BURVI	Q4bsv7 burkholderi
45	8	2.9	280	2	Q81D98_BACCR	Q81d98 bacillus ce

ALIGNMENTS

RESULT 1

R4RL2_HUMAN

ID R4RL2_HUMAN STANDARD; PRT; 420 AA.

AC Q86UN3; Q6X813;

DT 07-FEB-2006, integrated into UniProtKB/Swiss-Prot.

DT 01-JUN-2003, sequence version 1.

DT 07-MAR-2006, entry version 18.

DE Reticulon-4 receptor-like 2 precursor (Nogo-66 receptor homolog 1)

DE (Nogo-66 receptor-related protein 2) (NgR2) (Nogo receptor-like 3).

GN Name=RTN4RL2; Synonyms=NGRH1, NGRL3;

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;

OC Homo.

OX NCBI_TaxID=9606;

RN [1]

RP NUCLEOTIDE SEQUENCE [mRNA], SUBCELLULAR LOCATION, AND TISSUE

RP SPECIFICITY.

RC TISSUE=Brain;

RX MEDLINE=22581832; PubMed=12694398;

RA Pignot V., Hein A.E., Barske C., Wiessner C., Walmsley A.R.,

RA Kaupmann K., Mayeur H., Sommer B., Mir A.K., Frentzel S.;

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OM protein - protein search, using sw model

Run on: June 20, 2006, 10:08:00 ; Search time 152.373 Seconds
(without alignments)
930.199 Million cell updates/sec

Title: US-10-735-256-2_COPY_1_310
Perfect score: 1621
Sequence: 1 MLPGLRRLQAPASACLLM.....PPERQGRDLRALREADFQAC 310

Scoring table: BLOSUM62
Gapext 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_8:
1: geneseqp1980s:
2: geneseqp1990s:
3: geneseqp2000s:
4: geneseqp2001s:
5: geneseqp2002s:
6: geneseqp2003as:
7: geneseqp2003bs:
8: geneseqp2004s:
9: geneseqp2005s:
10: geneseqp2006s:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Score	Match	Length	DB	ID	Description
1	1621	100.0	401	7	ADF28528	Adf28528 NgRHyp mut
2	1621	100.0	420	5	AAO21477	Aao21477 Human NgR
3	1621	100.0	420	6	ABR55621	Abr55621 Amino aci
4	1621	100.0	420	7	ADF28510	Adf28510 NgRHyp pre
5	1621	100.0	420	8	ADS10516	Ads10516 Human the
6	1576	97.2	419	8	ADM72131	Adm72131 Human NTR
7	1568	96.7	420	6	ABR55628	Abr55628 Amino aci

8	1568	96.7	420	8	ADT77788	Adt77788 Rat Nogo
9	1568	96.7	452	8	ADT77808	Adt77808 Chimeric
10	1568	96.7	452	8	ADT77802	Adt77802 Chimeric
11	1568	96.7	474	8	ADT77796	Adt77796 Chimeric
12	1528	94.3	401	6	AAE33486	Aae33486 Human REM
13	1528	94.3	401	7	ADE07875	Ade07875 Novel pro
14	1512.5	93.3	512	7	ADC13559	Adc13559 Human NOV
15	1477	91.1	390	5	AAO21482	Aao21482 Mature hu
16	1477	91.1	390	7	ADF28529	Adf28529 NgRH _y mat
17	1460	90.1	286	8	ADT77787	Adt77787 Rat Nogo
18	1372.5	84.7	807	4	ABG15173	Abg15173 Novel hum
19	906.5	55.9	445	8	ADT77794	Adt77794 Rat Nogo
20	905.5	55.9	415	8	ADT77800	Adt77800 Chimeric
21	905.5	55.9	445	6	AAO27009	Aao27009 Rat NgRH ₂
22	905.5	55.9	445	8	ADN12049	Adn12049 Novel rat
23	905.5	55.9	445	8	ADT77790	Adt77790 Rat Nogo
24	903	55.7	461	5	AAO21478	Aao21478 Mouse NgR
25	901.5	55.6	441	6	AAO27001	Aao27001 Human NgR
26	901.5	55.6	441	8	ADN12047	Adn12047 Novel hum
27	901.5	55.6	473	8	ADT77795	Adt77795 Polypepti
28	879	54.2	421	5	AAO21483	Aao21483 Mature mo
29	791	48.8	392	5	AAO21487	Aao21487 Partial h
30	787	48.6	473	8	ADG75446	Adg75446 Macaque b
31	783	48.3	310	8	ADM33975	Adm33975 Human Nog
32	783	48.3	310	9	ADY34441	Ady34441 Human Nog
33	783	48.3	310	9	AEB19598	Aeb19598 Human Nog
34	783	48.3	344	8	ADM33974	Adm33974 Human Nog
35	783	48.3	344	8	ADU21101	Adu21101 Human Nog
36	783	48.3	344	9	ADY34440	Ady34440 Human Nog
37	783	48.3	344	9	AEB19597	Aeb19597 Human Nog
38	783	48.3	344	9	AEB86619	Aeb86619 Human NOG
39	783	48.3	472	3	AAB33426	Aab33426 Human PRO
40	783	48.3	473	2	AAY41745	Aay41745 Human PRO
41	783	48.3	473	3	AAB44301	Aab44301 Human PRO
42	783	48.3	473	3	AAB24410	Aab24410 Human PRO
43	783	48.3	473	3	AAY95345	Aay95345 Human PRO
44	783	48.3	473	4	AAU12362	Aau12362 Human PRO
45	783	48.3	473	4	AAU04589	Aau04589 Human Nog

ALIGNMENTS

RESULT 1

ADF28528

ID ADF28528 standard; protein; 401 AA.

XX

AC ADF28528;

XX

DT 12-FEB-2004 (first entry)

XX

DE NgRH_y mutant protein lacking transmembrane domain - SED ID 438.

XX

KW neuroprotective; nootropic; cerebroprotective; antiparkinsonian;
 KW neurological; spinal cord injury; cranial; cerebral trauma; stroke;
 KW Alzheimer's disease; anxiety; autism; Parkinson's; tardive dyskinesia;
 KW paralysis; seizure; memory disorder; adiponectin; Clq domain;

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OM protein - protein search, using sw model

Run on: June 20, 2006, 10:54:09 ; Search time 38.3559 Seconds
(without alignments)
707.439 Million cell updates/sec

Title: US-10-735-256-2_COPY_1_310
Perfect score: 1621
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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4: /EMC_Celerra_SIDS3/ptodata/2/iaa/H_COMB.pep:
5: /EMC_Celerra_SIDS3/ptodata/2/iaa/PCTUS_COMB.pep:
6: /EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query				Description
		Match	Length	DB	ID	
1	783	48.3	473	2	US-09-949-016-8448	Sequence 8448, App
2	783	48.3	473	2	US-09-999-833A-400	Sequence 400, App
3	783	48.3	473	2	US-10-020-445A-400	Sequence 400, App
4	783	48.3	473	2	US-09-978-189-400	Sequence 400, App
5	783	48.3	473	2	US-10-017-085A-400	Sequence 400, App
6	783	48.3	473	3	US-10-145-129A-400	Sequence 400, App
7	783	48.3	473	3	US-10-013-929A-400	Sequence 400, App
8	783	48.3	473	3	US-10-013-917A-400	Sequence 400, App
9	780	48.1	380	2	US-09-461-325-161	Sequence 161, App
10	780	48.1	380	2	US-10-012-542-161	Sequence 161, App

11	780	48.1	380	2	US-10-115-123-161	Sequence 161, Appl
12	369	22.8	481	2	US-09-853-753-2	Sequence 2, Appl
13	369	22.8	485	2	US-09-949-016-8704	Sequence 8704, Ap
14	357	22.0	545	3	US-10-114-270-38	Sequence 38, Appl
15	354	21.8	545	3	US-10-114-270-40	Sequence 40, Appl
16	353	21.8	605	2	US-09-063-950-5	Sequence 5, Appl
17	349.5	21.6	622	2	US-10-188-495-48	Sequence 48, Appl
18	349	21.5	605	1	US-08-190-802A-49	Sequence 49, Appl
19	349	21.5	605	2	US-08-477-346-49	Sequence 49, Appl
20	349	21.5	605	2	US-08-473-089-49	Sequence 49, Appl
21	349	21.5	605	2	US-08-487-072A-49	Sequence 49, Appl
22	349	21.5	605	2	US-09-538-092-1087	Sequence 1087, Ap
23	349	21.5	623	2	US-09-949-016-10995	Sequence 10995, A
24	345.5	21.3	673	2	US-09-063-950-2	Sequence 2, Appl
25	345.5	21.3	673	2	US-09-991-181-52	Sequence 52, Appl
26	345.5	21.3	673	2	US-09-990-444-52	Sequence 52, Appl
27	345.5	21.3	673	2	US-09-997-333-52	Sequence 52, Appl
28	345.5	21.3	673	2	US-09-992-598-52	Sequence 52, Appl
29	345.5	21.3	673	2	US-09-989-735-52	Sequence 52, Appl
30	345.5	21.3	673	3	US-09-989-726-52	Sequence 52, Appl
31	345.5	21.3	673	3	US-09-997-514-52	Sequence 52, Appl
32	345.5	21.3	673	3	US-09-989-728-52	Sequence 52, Appl
33	345.5	21.3	673	3	US-09-997-349-52	Sequence 52, Appl
34	345.5	21.3	673	3	US-09-997-653-52	Sequence 52, Appl
35	345.5	21.3	673	3	US-09-989-293A-52	Sequence 52, Appl
36	333.5	20.6	640	2	US-09-907-794A-292	Sequence 292, App
37	333.5	20.6	640	2	US-09-905-125A-292	Sequence 292, App
38	333.5	20.6	640	2	US-09-902-775A-292	Sequence 292, App
39	333.5	20.6	640	2	US-09-906-700-292	Sequence 292, App
40	333.5	20.6	640	2	US-09-903-603A-292	Sequence 292, App
41	333.5	20.6	640	2	US-09-904-920A-292	Sequence 292, App
42	333.5	20.6	640	2	US-09-909-064-292	Sequence 292, App
43	333.5	20.6	640	2	US-09-905-381A-292	Sequence 292, App
44	333.5	20.6	640	2	US-09-906-618-292	Sequence 292, App
45	333.5	20.6	640	2	US-09-906-646-292	Sequence 292, App

ALIGNMENTS

RESULT 1

US-09-949-016-8448
; Sequence 8448, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES
THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498

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OM protein - protein search, using sw model

Run on: June 20, 2006, 11:24:49 ; Search time 130.305 Seconds
(without alignments)
1102.003 Million cell updates/sec

Title: US-10-735-256-2_COPY_1_310
Perfect score: 1621
Sequence: 1 MLPGLRRLQAPASACLLM.....PPERQGRDLRALREADFQAC 310

Scoring table: BLOSUM62
Gapext 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep:
3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep:
4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep:
5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep:
6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pep:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1621	100.0	401	5	US-10-496-905-438 Sequence 438, App
2	1621	100.0	420	3	US-09-972-546-2 Sequence 2, Appli
3	1621	100.0	420	5	US-10-735-256-2 Sequence 2, Appli
4	1621	100.0	420	5	US-10-496-905-420 Sequence 420, App
5	1621	100.0	420	5	US-10-491-810A-2 Sequence 2, Appli
6	1568	96.7	420	5	US-10-491-810A-25 Sequence 25, Appl
7	1528	94.3	401	5	US-10-477-714-17 Sequence 17, Appl
8	1512.5	93.3	512	4	US-10-188-248-38 Sequence 38, Appl
9	1477	91.1	390	3	US-09-972-546-8 Sequence 8, Appli
10	1477	91.1	390	5	US-10-735-256-8 Sequence 8, Appli
11	1477	91.1	390	5	US-10-496-905-439 Sequence 439, App

12	1372.5	84.7	807	5	US-10-450-763-45532	Sequence 45532, A
13	905.5	55.9	445	5	US-10-487-886-25	Sequence 25, Appl
14	903	55.7	461	3	US-09-972-546-4	Sequence 4, Appli
15	903	55.7	461	5	US-10-735-256-4	Sequence 4, Appli
16	901.5	55.6	441	5	US-10-487-886-2	Sequence 2, Appli
17	879	54.2	421	3	US-09-972-546-9	Sequence 9, Appli
18	879	54.2	421	5	US-10-735-256-9	Sequence 9, Appli
19	791	48.8	392	3	US-09-972-546-14	Sequence 14, Appl
20	791	48.8	392	5	US-10-735-256-14	Sequence 14, Appl
21	787	48.6	473	4	US-10-271-078-7	Sequence 7, Appli
22	783	48.3	310	6	US-11-055-163-7	Sequence 7, Appli
23	783	48.3	344	6	US-11-055-163-6	Sequence 6, Appli
24	783	48.3	473	3	US-09-758-140-2	Sequence 2, Appli
25	783	48.3	473	3	US-09-893-348-26	Sequence 26, Appl
26	783	48.3	473	3	US-09-972-599A-2	Sequence 2, Appli
27	783	48.3	473	3	US-09-978-295A-400	Sequence 400, App
28	783	48.3	473	3	US-09-978-697-400	Sequence 400, App
29	783	48.3	473	3	US-09-978-192A-400	Sequence 400, App
30	783	48.3	473	3	US-09-999-832A-400	Sequence 400, App
31	783	48.3	473	3	US-09-978-189-400	Sequence 400, App
32	783	48.3	473	3	US-09-978-608A-400	Sequence 400, App
33	783	48.3	473	3	US-09-978-585A-400	Sequence 400, App
34	783	48.3	473	3	US-09-978-191A-400	Sequence 400, App
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36	783	48.3	473	3	US-09-978-564A-400	Sequence 400, App
37	783	48.3	473	3	US-09-999-833A-400	Sequence 400, App
38	783	48.3	473	3	US-09-981-915A-400	Sequence 400, App
39	783	48.3	473	3	US-09-978-824-400	Sequence 400, App
40	783	48.3	473	3	US-09-918-585A-400	Sequence 400, App
41	783	48.3	473	3	US-09-999-834A-400	Sequence 400, App
42	783	48.3	473	3	US-09-978-423A-400	Sequence 400, App
43	783	48.3	473	3	US-09-978-193A-400	Sequence 400, App
44	783	48.3	473	3	US-09-999-830A-400	Sequence 400, App
45	783	48.3	473	3	US-09-978-757A-400	Sequence 400, App

ALIGNMENTS

RESULT 1

US-10-496-905-438

; Sequence 438, Application US/10496905

; Publication No. US20050192215A1

; GENERAL INFORMATION:

; APPLICANT: Ghosh, Malabika

; APPLICANT: Tang, Y. Tom

; APPLICANT: Wang, Jian-Rui

; APPLICANT: Wang, Zhiwei

; APPLICANT: Zhao, Qing

; APPLICANT: Xu, Chongjun

; APPLICANT: Mulero, Julio J

; APPLICANT: Boyle, Bryan J.

; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES

; FILE REFERENCE: HYS-B1CIP/US

; CURRENT APPLICATION NUMBER: US/10/496,905

; CURRENT FILING DATE: 2004-05-26

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OM protein - protein search, using sw model

Run on: June 20, 2006, 11:26:34 ; Search time 6.83051 Seconds
(without alignments)
1023.724 Million cell updates/sec

Title: US-10-735-256-2_COPY_1_310
Perfect score: 1621
Sequence: 1 MLPGLRLLLQAPASACLLM..... PPERQGRDLRALREADFQAC 310

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 96747 seqs, 22556637 residues

Total number of hits satisfying chosen parameters: 96747

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA_New:
1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_NEW_PUB.pep:
2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US06_NEW_PUB.pep:
3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_NEW_PUB.pep:
4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_NEW_PUB.pep:
5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/PCT_NEW_PUB.pep:
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7: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_NEW_PUB.pep:
8: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US60_NEW_PUB.pep:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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1	359	22.1	811	6	US-10-505-928-32		Sequence 32, Appl
2	359	22.1	811	6	US-10-505-928-87		Sequence 87, Appl
3	345.5	21.3	673	7	US-11-101-316-16		Sequence 16, Appl
4	311.5	19.2	294	6	US-10-505-928-33		Sequence 33, Appl
5	295	18.2	1523	6	US-10-196-749-290		Sequence 290, App
6	288	17.8	513	7	US-11-101-316-124		Sequence 124, App
7	280	17.3	370	7	US-11-293-697-3248		Sequence 3248, Ap
8	279	17.2	598	7	US-11-296-092-69		Sequence 69, Appl
9	275.5	17.0	649	6	US-10-196-749-384		Sequence 384, App

10	275.5	17.0	649	7	US-11-101-316-132	Sequence 132, App
11	267.5	16.5	812	6	US-10-518-039-5	Sequence 5, Appli
12	266	16.4	716	6	US-10-518-039-6	Sequence 6, Appli
13	250	15.4	719	7	US-11-293-697-3841	Sequence 3841, Ap
14	248	15.3	359	6	US-10-933-854-18	Sequence 18, Appli
15	234.5	14.5	557	6	US-10-196-749-326	Sequence 326, App
16	232	14.3	745	7	US-11-293-697-3826	Sequence 3826, Ap
17	226.5	14.0	611	6	US-10-520-783-2	Sequence 2, Appli
18	218.5	13.5	531	7	US-11-257-581-4	Sequence 4, Appli
19	218.5	13.5	544	7	US-11-257-581-1	Sequence 1, Appli
20	218.5	13.5	544	7	US-11-257-581-2	Sequence 2, Appli
21	218	13.4	531	7	US-11-257-581-5	Sequence 5, Appli
22	218	13.4	531	7	US-11-257-581-6	Sequence 6, Appli
23	218	13.4	544	7	US-11-257-581-3	Sequence 3, Appli
24	217.5	13.4	379	7	US-11-296-092-2	Sequence 2, Appli
25	203	12.5	290	7	US-11-257-581-10	Sequence 10, Appli
26	203	12.5	302	7	US-11-257-581-7	Sequence 7, Appli
27	203	12.5	302	7	US-11-257-581-8	Sequence 8, Appli
28	202.5	12.5	290	7	US-11-257-581-11	Sequence 11, Appli
29	202.5	12.5	290	7	US-11-257-581-12	Sequence 12, Appli
30	202.5	12.5	301	7	US-11-257-581-9	Sequence 9, Appli
31	202.5	12.5	368	6	US-10-505-928-743	Sequence 743, App
32	189.5	11.7	703	7	US-11-291-140-4	Sequence 4, Appli
33	189.5	11.7	904	7	US-11-144-322-2	Sequence 2, Appli
34	189.5	11.7	904	7	US-11-291-140-2	Sequence 2, Appli
35	187	11.5	977	6	US-10-449-902-50526	Sequence 50526, A
36	180.5	11.1	692	6	US-10-196-749-560	Sequence 560, App
37	178.5	11.0	616	6	US-10-196-749-158	Sequence 158, App
38	178.5	11.0	1032	6	US-10-196-749-552	Sequence 552, App
39	171.5	10.6	1123	6	US-10-953-349-4749	Sequence 4749, Ap
40	171	10.5	298	7	US-11-297-134-25	Sequence 25, Appli
41	170.5	10.5	1074	6	US-10-449-902-52953	Sequence 52953, A
42	169	10.4	1135	6	US-10-449-902-56546	Sequence 56546, A
43	168.5	10.4	501	6	US-10-449-902-48020	Sequence 48020, A
44	168	10.4	964	6	US-10-449-902-47345	Sequence 47345, A
45	167	10.3	546	6	US-10-196-749-412	Sequence 412, App

ALIGNMENTS

RESULT 1

US-10-505-928-32
; Sequence 32, Application US/10505928
; Publication No. US20060088532A1
; GENERAL INFORMATION:
; APPLICANT: Ludwig Institute for Cancer Research et al.
; TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
; FILE REFERENCE: 28967/39178
; CURRENT APPLICATION NUMBER: US/10/505,928
; CURRENT FILING DATE: 2004-08-27
; PRIOR APPLICATION NUMBER: US 60/363,019
; PRIOR FILING DATE: 2002-03-07
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; SOFTWARE: PatentIn 3.2
; SEQ ID NO 32
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